

1652
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APR 03 2002

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/040,655

DATE: 01/24/2002

TIME: 16:16:27

TECH CENTER 1600/2900

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF3\01242002\J040655.raw

ENTERED

3 <110> APPLICANT: Andrade-Gordon, Patricia
4 Darrow, Andrew
5 Qi, Jian-shen
7 <120> TITLE OF INVENTION: DNA encoding the novel human serine
8 protease T
10 <130> FILE REFERENCE: ORT-1032
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/040,655
C--> 13 <141> CURRENT FILING DATE: 2002-01-07
15 <160> NUMBER OF SEQ ID NOS: 11
17 <170> SOFTWARE: PatentIn Ver. 2.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1110
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
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26 tctgtctgct gctgtgtttt ggggtctcaga gggccaaggc agcaacagcc tgttgtcgcc 120
27 ccaggatgct gaaccgaatg gtgggcgggc aggacacgca ggagggcgag tggccctggc 180
28 aagtcagcat ccagcgcaac ggaagccact tctgcggggg cagcctcatc gcggagcagt 240
29 gggctctgac ggctgcgcac tgcttccgca acacctctga gacgtccctg taccaggtcc 300
30 tgctgggggc aaggcagcta gtgcagccgg gaccacacgc tatgtatgcc cgggtgaggc 360
31 aggtggagag caacccctg taccagggca cggcctccag cgctgacgtg gccctggtgg 420
32 agctggaggc accagtgcct ttcaccaatt acatcctccc cgtgtgcctg cctgaccctc 480
33 cggtgatctt tgagacgggc atgaactgct gggtcactgg ctggggcagc cccagtgagg 540
34 aagacctcct gcccgaaacc cggatcctgc agaaactcgc tgtgccatc atcgacacac 600
35 ccaagtgcaa cctgctctac agcaaagaca ccgagtttgg ctaccaaccc aaaaccatca 660
36 agaattgacat gctgtgcgcc ggcttcgagg agggcaagaa ggatgcctgc aagggcgact 720
37 cgggcggccc cctggtgtgc ctctgtgggc agtcgtggct gcaggcgggg gtgatcagct 780
38 ggggtgaggg ctgtgccgc cagaaccgcc cagggtgtcta catccgtgtc accgcccacc 840
39 acaactggat ccattcgatc atcccaaac tgcagttcca gccagcgagg ttgggcggcc 900
40 agaagtgaga ccccgggggc caggagcccc ttgagcagag ctctgcaccc agcctgcccc 960
41 cccacaccat cctgtgtgtc ctcccagcgc tgetgttgca cctgtgagcc ccaccagact 1020
42 catttgtaaa tagcgtcct tctcccctc tcaaataccc ttattttatt tatgtttctc 1080
43 ccaataaaaa cccagcctgt gtgccagctg 1110
45 <210> SEQ ID NO: 2
46 <211> LENGTH: 20
47 <212> TYPE: DNA
48 <213> ORGANISM: Artificial Sequence
50 <220> FEATURE:
51 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
53 <400> SEQUENCE: 2
54 gccaggcctg aggacatgag 20
56 <210> SEQ ID NO: 3

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57 <211> LENGTH: 20
58 <212> TYPE: DNA
59 <213> ORGANISM: Artificial Sequence
61 <220> FEATURE:
62 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
64 <400> SEQUENCE: 3
65 tgcgctggat gctgacttgc                                20
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68 <211> LENGTH: 40
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70 <213> ORGANISM: Artificial Sequence
72 <220> FEATURE:
73 <223> OTHER INFORMATION: Description of Artificial Sequence: Nested probe
75 <400> SEQUENCE: 4
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79 <211> LENGTH: 30
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81 <213> ORGANISM: Artificial Sequence
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84 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
86 <400> SEQUENCE: 5
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90 <211> LENGTH: 30
91 <212> TYPE: DNA
92 <213> ORGANISM: Artificial Sequence
94 <220> FEATURE:
95 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
97 <400> SEQUENCE: 6
98 ggggtctaga cttctggccg cccaacctcg                    30
100 <210> SEQ ID NO: 7
101 <211> LENGTH: 290
102 <212> TYPE: PRT
103 <213> ORGANISM: Homo sapiens
105 <400> SEQUENCE: 7
106 Met Arg Arg Pro Ala Ala Val Pro Leu Leu Leu Leu Cys Phe Gly
107 1          5          10          15
109 Ser Gln Arg Ala Lys Ala Ala Thr Ala Cys Gly Arg Pro Arg Met Leu
110          20          25          30
112 Asn Arg Met Val Gly Gly Gln Asp Thr Gln Glu Gly Glu Trp Pro Trp
113          35          40          45
115 Gln Val Ser Ile Gln Arg Asn Gly Ser His Phe Cys Gly Gly Ser Leu
116          50          55          60
118 Ile Ala Glu Gln Trp Val Leu Thr Ala Ala His Cys Phe Arg Asn Thr
119 65          70          75          80
121 Ser Glu Thr Ser Leu Tyr Gln Val Leu Leu Gly Ala Arg Gln Leu Val
122          85          90          95
124 Gln Pro Gly Pro His Ala Met Tyr Ala Arg Val Arg Gln Val Glu Ser

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125          100          105          110
127 Asn Pro Leu Tyr Gln Gly Thr Ala Ser Ser Ala Asp Val Ala Leu Val
128          115          120          125
130 Glu Leu Glu Ala Pro Val Pro Phe Thr Asn Tyr Ile Leu Pro Val Cys
131          130          135          140
133 Leu Pro Asp Pro Ser Val Ile Phe Glu Thr Gly Met Asn Cys Trp Val
134 145          150          155          160
136 Thr Gly Trp Gly Ser Pro Ser Glu Glu Asp Leu Leu Pro Glu Pro Arg
137          165          170          175
139 Ile Leu Gln Lys Leu Ala Val Pro Ile Ile Asp Thr Pro Lys Cys Asn
140          180          185          190
142 Leu Leu Tyr Ser Lys Asp Thr Glu Phe Gly Tyr Gln Pro Lys Thr Ile
143          195          200          205
145 Lys Asn Asp Met Leu Cys Ala Gly Phe Glu Glu Gly Lys Lys Asp Ala
146          210          215          220
148 Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Leu Val Gly Gln Ser
149 225          230          235          240
151 Trp Leu Gln Ala Gly Val Ile Ser Trp Gly Glu Gly Cys Ala Arg Gln
152          245          250          255
154 Asn Arg Pro Gly Val Tyr Ile Arg Val Thr Ala His His Asn Trp Ile
155          260          265          270
157 His Arg Ile Ile Pro Lys Leu Gln Phe Gln Pro Ala Arg Leu Gly Gly
158          275          280          285
160 Gln Lys
161          290

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164 <210> SEQ ID NO: 8

165 <211> LENGTH: 1130

166 <212> TYPE: DNA

167 <213> ORGANISM: Artificial Sequence

169 <220> FEATURE:

170 <223> OTHER INFORMATION: Description of Artificial Sequence: Fusion gene of
171 Protease T in a zymogen activation vector

173 <400> SEQUENCE: 8

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174 gaattcacca ccatggacag caaagggttcg tcgcagaaat cccgcctgct cctgctgctg 60
175 gtggtgtcaa atctactctt gtgccagggt gtggtctccg actacaagga cgacgacgac 120
176 gtggacgcgg ccgctcttgc tgcccccttt gatgatgatg acaagatcgt tgggggctat 180
177 gctctagagg agggcgagtg gccctggcaa gtcagcatcc agcgcaacgg aagccacttc 240
178 tgcgggggca gcctcatcgc ggagcagtggt gtccctgacgg ctgcgcactg cttccgcaac 300
179 acctctgaga cgctccctgta ccaggtcctg ctggggggcaa ggcagctagt gcagccggga 360
180 ccacacgcta tgtatgcccg ggtgaggcag gtggagagca accccctgta ccagggcacg 420
181 gcctccagcg ctgacgtggc cctggtggag ctggaggcac cagtgccctt caccaattac 480
182 atcctccccg tgtgcctgcc tgaccctcgc gtgatctttg agacgggcat gaactgctgg 540
183 gtcactggct ggggcagccc cagtgaggaa gacctcctgc ccgaaccgcg gatcctgcag 600
184 aaactcgctg tgcccatcat cgacacaccc aagtgaacc tgctctacag caaagacacc 660
185 gagtttggtt accaacccaa aaccatcaag aatgacatgc tgtgcgccgg ctctgaggag 720
186 ggcaagaagg atgcctgcaa gggcgactcg ggcgccccc tgggtgtgct cgtgggtcag 780
187 tcgtggctgc aggcgggggt gatcagctgg ggtgagggt gtgcccggca gaaccggcca 840
188 ggtgtctaca tccgtgtcac cgcccaccac aactggatcc atcggatcat ccccaaactg 900
189 cagttccagc cagcgagggt gggcgccag aagtctagac atcaccatca ccatcactag 960

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190 cggccgcttc cctttagtga gggttaatgc ttcgagcaga catgataaga tacattgatg 1020
191 agtttggaca aaccacaact agaatgcagt gaaaaaaatg ctttatttgt gaaatttgtg 1080
192 atgctattgc tttatttgta accattataa gctgcaataa acaagttgac 1130
194 <210> SEQ ID NO: 9
195 <211> LENGTH: 315
196 <212> TYPE: PRT
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein
201 of Protease T in a zymogen activation construct
203 <400> SEQUENCE: 9
204 Met Asp Ser Lys Gly Ser Ser Gln Lys Ser Arg Leu Leu Leu Leu Leu
205 1 5 10 15
207 Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser Asp Tyr Lys
208 20 25 30
210 Asp Asp Asp Asp Val Asp Ala Ala Leu Ala Ala Pro Phe Asp Asp
211 35 40 45
213 Asp Asp Lys Ile Val Gly Gly Tyr Ala Leu Glu Glu Gly Glu Trp Pro
214 50 55 60
216 Trp Gln Val Ser Ile Gln Arg Asn Gly Ser His Phe Cys Gly Gly Ser
217 65 70 75 80
219 Leu Ile Ala Glu Gln Trp Val Leu Thr Ala Ala His Cys Phe Arg Asn
220 85 90 95
222 Thr Ser Glu Thr Ser Leu Tyr Gln Val Leu Leu Gly Ala Arg Gln Leu
223 100 105 110
225 Val Gln Pro Gly Pro His Ala Met Tyr Ala Arg Val Arg Gln Val Glu
226 115 120 125
228 Ser Asn Pro Leu Tyr Gln Gly Thr Ala Ser Ser Ala Asp Val Ala Leu
229 130 135 140
231 Val Glu Leu Glu Ala Pro Val Pro Phe Thr Asn Tyr Ile Leu Pro Val
232 145 150 155 160
234 Cys Leu Pro Asp Pro Ser Val Ile Phe Glu Thr Gly Met Asn Cys Trp
235 165 170 175
237 Val Thr Gly Trp Gly Ser Pro Ser Glu Glu Asp Leu Leu Pro Glu Pro
238 180 185 190
240 Arg Ile Leu Gln Lys Leu Ala Val Pro Ile Ile Asp Thr Pro Lys Cys
241 195 200 205
243 Asn Leu Leu Tyr Ser Lys Asp Thr Glu Phe Gly Tyr Gln Pro Lys Thr
244 210 215 220
246 Ile Lys Asn Asp Met Leu Cys Ala Gly Phe Glu Glu Gly Lys Lys Asp
247 225 230 235 240
249 Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Leu Val Gly Gln
250 245 250 255
252 Ser Trp Leu Gln Ala Gly Val Ile Ser Trp Gly Glu Gly Cys Ala Arg
253 260 265 270
255 Gln Asn Arg Pro Gly Val Tyr Ile Arg Val Thr Ala His His Asn Trp
256 275 280 285
258 Ile His Arg Ile Ile Pro Lys Leu Gln Phe Gln Pro Ala Arg Leu Gly
259 290 295 300

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261 Gly Gln Lys Ser Arg His His His His His

262 305 310 315

264 <210> SEQ ID NO: 10

265 <211> LENGTH: 4

266 <212> TYPE: PRT

267 <213> ORGANISM: Artificial Sequence

269 <220> FEATURE:

270 <223> OTHER INFORMATION: Description of Artificial Sequence: peptide substrate

272 <400> SEQUENCE: 10

273 Ala Ala Pro Phe

275 <210> SEQ ID NO: 11

276 <211> LENGTH: 4

277 <212> TYPE: PRT

278 <213> ORGANISM: Artificial Sequence

280 <220> FEATURE:

281 <223> OTHER INFORMATION: Description of Artificial Sequence: peptide substrate

283 <400> SEQUENCE: 11

284 Ala Ala Pro Val

VERIFICATION SUMMARY

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DATE: 01/24/2002

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Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF3\01242002\J040655.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date